

Exhibit C



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

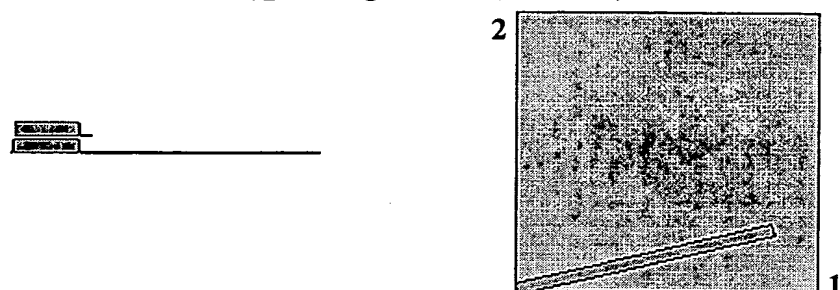
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

 Match: Mismatch: gap open: gap extension:

 x_dropoff: expect: wordsize: Filter ☒


Sequence 1 lcl|seq_1 Length 1414 (1 .. 1414)

Sequence 2 lcl|seq_2 Length 5540 (1 .. 5540)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2286 bits (1189), Expect = 0.0

Identities = 1191/1192 (99%)

Strand = Plus / Plus

SEQ ID NO: 1

AF279145

```

Query: 1      ,aggacccgcgaggaagggcccgcgatggcgcgctccctgagggtcgtggcgagttcgcg 60
              |||
Sbjct: 41      aggacccgcgaggaagggcccgcgatggcgcgctccctgagggtcgtggcgagttcgcg 100

Query: 61      agcgtgggaaggagcggaccctgctctccccgggctgcgggccatggccacggcgagcg 120
              |||
Sbjct: 101     agcgtgggaaggagcggaccctgctctccccgggctgcgggccatggccacggcgagcg 160

Query: 121     gagagccctcggcacggttccagtggtctctttggccactctggtgctcatctgcgc 180
              |||
Sbjct: 161     gagagccctcggcacggttccagtggtctctttggccactctggtgctcatctgcgc 220

Query: 181     cgggcaagggggacgcagggaggatgggggtccagcctgctacggcggatttgacctgta 240
              |||
Sbjct: 221     cgggcaagggggacgcagggaggatgggggtccagcctgctacggcggatttgacctgta 280
  
```

Query: 241 cttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgt 300
|||||
Sbjct: 281 cttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgt 340

Query: 301 ggaacagttggctcacaattcatcagcccacagttgagaatgtcctttattgttttctc 360
|||||
Sbjct: 341 ggaacagttggctcacaattcatcagcccacagttgagaatgtcctttattgttttctc 400

Query: 361 caccgaggaacaaccttaatgaaactgacagaagacagagaacaaatccgtcaaggcct 420
|||||
Sbjct: 401 caccgaggaacaaccttaatgaaactgacagaagacagagaacaaatccgtcaaggcct 460

Query: 421 agaagaactccagaaagttctgccaggaggagacacttacatgcatgaaggatttgaaag 480
|||||
Sbjct: 461 agaagaactccagaaagttctgccaggaggagacacttacatgcatgaaggatttgaaag 520

Query: 481 ggccagtgagcagatttattatgaaaacagacaagggtacaggacagccagcgtcatcat 540
|||||
Sbjct: 521 ggccagtgagcagatttattatgaaaacagacaagggtacaggacagccagcgtcatcat 580

Query: 541 tgctttgactgatggagaactccatgaagatctctttttctattcagagagggaggctaa 600
|||||
Sbjct: 581 tgctttgactgatggagaactccatgaagatctctttttctattcagagagggaggctaa 640

Query: 601 taggtctcgagatcttggtgcaattgtttactgtgttggtgtgaaagatttcaatgagac 660
|||||
Sbjct: 641 taggtctcgagatcttggtgcaattgtttactgtgttggtgtgaaagatttcaatgagac 700

Query: 661 acagctggcccggattgcgacagtaaggatcatgtgtttccgtgaatgacggccttca 720
|||||
Sbjct: 701 acagctggcccggattgcgacagtaaggatcatgtgtttccgtgaatgacggccttca 760

Query: 721 ggctctgcaaggcatcatccactcaattttgaagaagtctgcacgaaattctagcagc 780
|||||
Sbjct: 761 ggctctgcaaggcatcatccactcaattttgaagaagtctgcacgaaattctagcagc 820

Query: 781 tgaaccatccaccatagtgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt 840
|||||
Sbjct: 821 tgaaccatccaccatagtgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt 880

Query: 841 ccgacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcac 900
|||||
Sbjct: 881 ccgacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcac 940

Query: 901 actcaatgagaagcccttttctgtggaagacacttatttactgtgtccagcgcctatctt 960
|||||
Sbjct: 941 actcaatgagaagcccttttctgtggaagatacttatttactgtgtccagcgcctatctt 1000

Query: 961 aaaagaagttggcatgaaagctgcactccaggtcagcatgaacgatggcctctcttttat 1020
|||||
Sbjct: 1001 aaaagaagttggcatgaaagctgcactccaggtcagcatgaacgatggcctctcttttat 1060

Query: 1021 ctccagttctgtcatcatcaccaccacacactgttctgacggttccatcctggccatcgc 1080
|||||
Sbjct: 1061 ctccagttctgtcatcatcaccaccacacactgttctgacggttccatcctggccatcgc 1120

Query: 1081 cctgctgatcctgttcctgctcctagccctggctctcctctggtggttctggcccctctg 1140
|||||
Sbjct: 1121 cctgctgatcctgttcctgctcctagccctggctctcctctggtggttctggcccctctg 1180

Query: 1141 ctgcactgtgattatcaaggaggtccctccacccctgccgaggagagtggag 1192
|||||
Sbjct: 1181 ctgcactgtgattatcaaggaggtccctccacccctgccgaggagagtggag 1232

CPU time: 0.01 user secs. 0.02 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 8
Number of Sequences: 0
Number of extensions: 8
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1414
length of database: 10,224,276,066
effective HSP length: 25
effective length of query: 1389
effective length of database: 10,224,276,041
effective search space: 14201519420949
effective search space used: 14201519420949
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)